



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 08:47 am GMT

PDB ID : 2OU1
Title : Structures of apolipoprotein A-II and a lipid surrogate complex provide insights into apolipoprotein-lipid interactions
Authors : Kumar, M.S.; Carson, M.C.; Hussain, M.M.; Murthy, H.M.K.
Deposited on : 2007-02-09
Resolution : 2.00 Å (reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

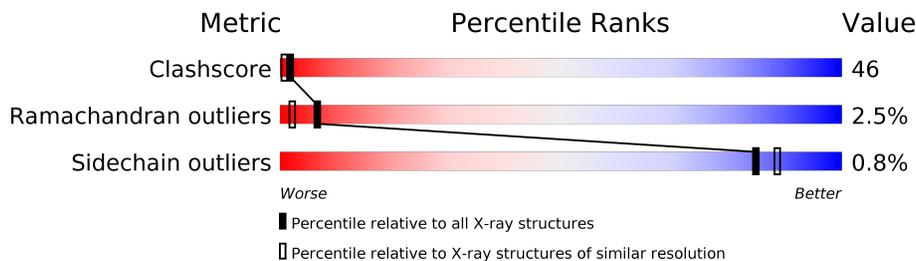
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	77	
1	B	77	
1	C	77	
1	D	77	
1	E	77	
1	F	77	
1	G	77	

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Mol	Chain	Length	Quality of chain
1	H	77	 40% 49% 6%
1	I	77	 34% 57% 6%
1	J	77	 43% 44% 9%
1	K	77	 44% 49% 5%
1	L	77	 39% 53% 6%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7397 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Apolipoprotein A-II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	72	Total 569	C 365	N 86	O 116	S 2	0	0	0
1	B	71	Total 560	C 360	N 85	O 113	S 2	0	0	0
1	C	73	Total 580	C 374	N 87	O 117	S 2	0	0	0
1	D	72	Total 573	C 369	N 86	O 116	S 2	0	0	0
1	E	72	Total 569	C 365	N 86	O 116	S 2	0	0	0
1	F	71	Total 560	C 360	N 85	O 113	S 2	0	0	0
1	G	73	Total 580	C 374	N 87	O 117	S 2	0	0	0
1	H	72	Total 573	C 369	N 86	O 116	S 2	0	0	0
1	I	72	Total 569	C 365	N 86	O 116	S 2	0	0	0
1	J	70	Total 553	C 355	N 84	O 112	S 2	0	0	0
1	K	73	Total 580	C 374	N 87	O 117	S 2	0	0	0
1	L	72	Total 573	C 369	N 86	O 116	S 2	0	0	0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	55	Total 55	O 55	0	0
2	B	39	Total 39	O 39	0	0

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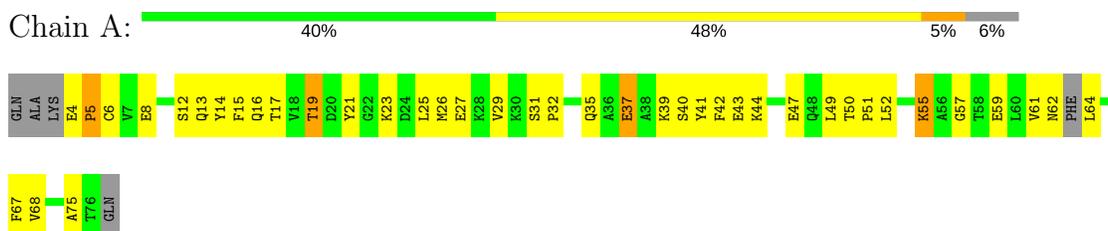
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	51	Total 51	O 51	0	0
2	D	38	Total 38	O 38	0	0
2	E	40	Total 40	O 40	0	0
2	F	47	Total 47	O 47	0	0
2	G	48	Total 48	O 48	0	0
2	H	40	Total 40	O 40	0	0
2	I	34	Total 34	O 34	0	0
2	J	50	Total 50	O 50	0	0
2	K	62	Total 62	O 62	0	0
2	L	54	Total 54	O 54	0	0

3 Residue-property plots [i](#)

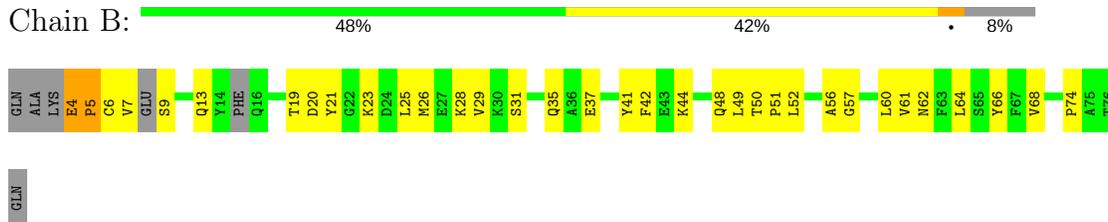
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

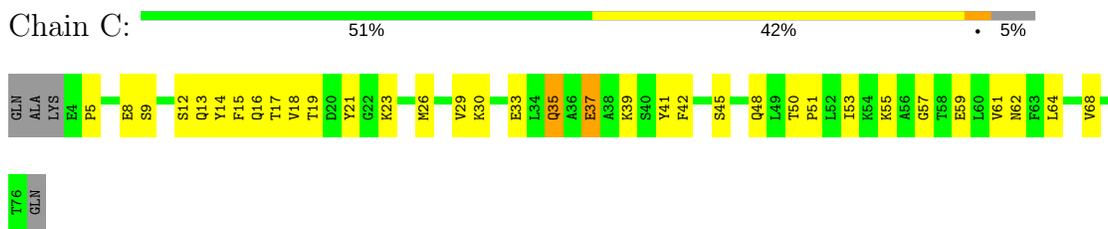
- Molecule 1: Apolipoprotein A-II



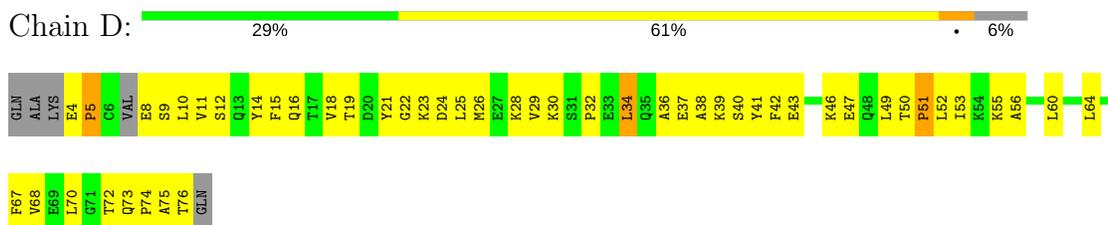
- Molecule 1: Apolipoprotein A-II



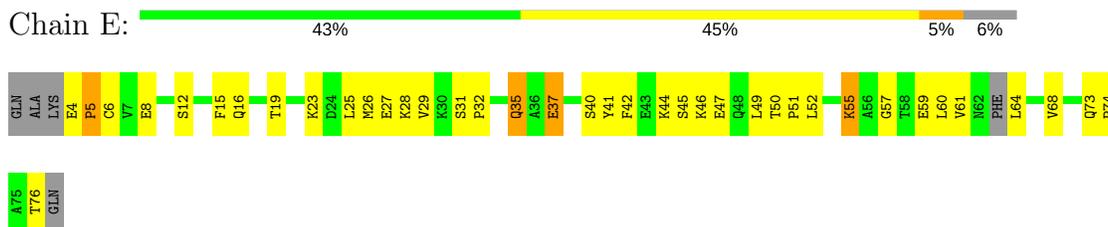
- Molecule 1: Apolipoprotein A-II



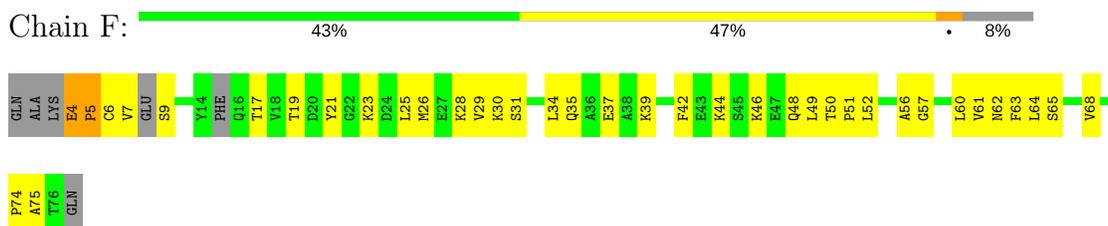
- Molecule 1: Apolipoprotein A-II



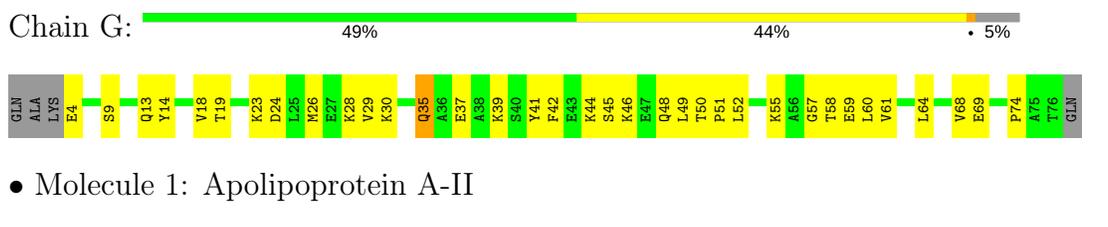
- Molecule 1: Apolipoprotein A-II



- Molecule 1: Apolipoprotein A-II



- Molecule 1: Apolipoprotein A-II



- Molecule 1: Apolipoprotein A-II



- Molecule 1: Apolipoprotein A-II



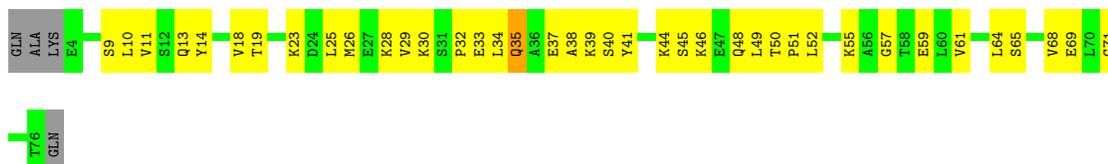
- Molecule 1: Apolipoprotein A-II





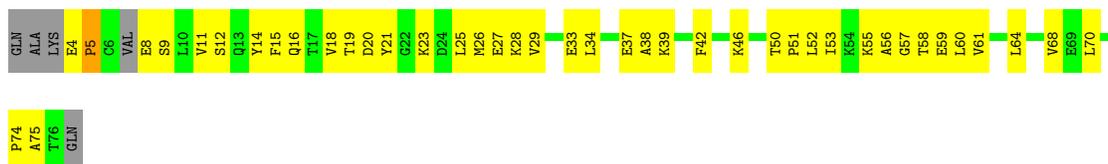
- Molecule 1: Apolipoprotein A-II

Chain K: 44% (Green), 49% (Yellow), 5% (Red)



- Molecule 1: Apolipoprotein A-II

Chain L: 39% (Green), 53% (Yellow), 6% (Red)



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.90Å 125.70Å 55.30Å 90.00° 93.40° 90.00°	Depositor
Resolution (Å)	8.00 – 2.00	Depositor
% Data completeness (in resolution range)	93.0 (8.00-2.00)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.187 , 0.219	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	7397	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.40	1/578 (0.2%)	0.55	0/779
1	B	0.41	1/568 (0.2%)	0.61	1/764 (0.1%)
1	C	0.49	2/591 (0.3%)	0.59	1/798 (0.1%)
1	D	0.42	1/583 (0.2%)	0.59	0/785
1	E	0.40	1/578 (0.2%)	0.55	0/779
1	F	0.40	1/568 (0.2%)	0.62	1/764 (0.1%)
1	G	0.45	1/591 (0.2%)	0.58	0/798
1	H	0.42	1/583 (0.2%)	0.59	0/785
1	I	0.40	1/578 (0.2%)	0.56	0/779
1	J	0.40	1/561 (0.2%)	0.60	1/754 (0.1%)
1	K	0.47	1/591 (0.2%)	0.56	0/798
1	L	0.42	1/583 (0.2%)	0.55	0/785
All	All	0.42	13/6953 (0.2%)	0.58	4/9368 (0.0%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	37	GLU	CD-OE2	7.02	1.33	1.25
1	H	37	GLU	CD-OE2	6.94	1.33	1.25
1	C	37	GLU	CD-OE2	6.91	1.33	1.25
1	B	37	GLU	CD-OE2	6.89	1.33	1.25
1	I	37	GLU	CD-OE2	6.89	1.33	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	4	GLU	C-N-CD	-8.87	101.08	120.60
1	B	4	GLU	C-N-CD	-8.76	101.33	120.60
1	J	4	GLU	C-N-CD	-8.72	101.41	120.60
1	C	15	PHE	CB-CA-C	5.35	121.09	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	569	0	568	64	0
1	B	560	0	561	39	0
1	C	580	0	578	52	0
1	D	573	0	568	93	0
1	E	569	0	568	69	0
1	F	560	0	561	47	0
1	G	580	0	578	45	0
1	H	573	0	568	82	0
1	I	569	0	568	80	0
1	J	553	0	552	55	0
1	K	580	0	578	55	1
1	L	573	0	568	68	0
2	A	55	0	0	27	0
2	B	39	0	0	14	0
2	C	51	0	0	41	0
2	D	38	0	0	28	0
2	E	40	0	0	23	0
2	F	47	0	0	21	0
2	G	48	0	0	25	0
2	H	40	0	0	33	0
2	I	34	0	0	29	0
2	J	50	0	0	35	0
2	K	62	0	0	42	0
2	L	54	0	0	31	0
All	All	7397	0	6816	633	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 46.

The worst 5 of 633 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:47:GLU:HA	2:E:97:HOH:O	1.27	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:23:LYS:HA	2:I:98:HOH:O	1.32	1.26
1:I:26:MET:HE2	2:L:101:HOH:O	1.35	1.26
1:F:34:LEU:HD13	2:F:81:HOH:O	1.32	1.25
1:I:67:PHE:HB3	2:I:85:HOH:O	1.35	1.24

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:28:LYS:CE	1:K:69:GLU:OE1[2_546]	2.16	0.04

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	68/77 (88%)	58 (85%)	7 (10%)	3 (4%)	3	1
1	B	65/77 (84%)	57 (88%)	7 (11%)	1 (2%)	12	5
1	C	71/77 (92%)	65 (92%)	5 (7%)	1 (1%)	13	6
1	D	68/77 (88%)	62 (91%)	5 (7%)	1 (2%)	12	5
1	E	68/77 (88%)	59 (87%)	6 (9%)	3 (4%)	3	1
1	F	65/77 (84%)	58 (89%)	6 (9%)	1 (2%)	12	5
1	G	71/77 (92%)	66 (93%)	4 (6%)	1 (1%)	13	6
1	H	68/77 (88%)	61 (90%)	5 (7%)	2 (3%)	5	1
1	I	68/77 (88%)	60 (88%)	5 (7%)	3 (4%)	3	1
1	J	64/77 (83%)	60 (94%)	3 (5%)	1 (2%)	11	5
1	K	71/77 (92%)	66 (93%)	4 (6%)	1 (1%)	13	6
1	L	68/77 (88%)	61 (90%)	5 (7%)	2 (3%)	5	1
All	All	815/924 (88%)	733 (90%)	62 (8%)	20 (2%)	6	2

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	PRO
1	B	5	PRO
1	D	5	PRO
1	E	5	PRO
1	F	5	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	65/69 (94%)	63 (97%)	2 (3%)	45	44
1	B	64/69 (93%)	64 (100%)	0	100	100
1	C	66/69 (96%)	66 (100%)	0	100	100
1	D	65/69 (94%)	63 (97%)	2 (3%)	45	44
1	E	65/69 (94%)	64 (98%)	1 (2%)	70	74
1	F	64/69 (93%)	64 (100%)	0	100	100
1	G	66/69 (96%)	66 (100%)	0	100	100
1	H	65/69 (94%)	64 (98%)	1 (2%)	70	74
1	I	65/69 (94%)	65 (100%)	0	100	100
1	J	63/69 (91%)	63 (100%)	0	100	100
1	K	66/69 (96%)	66 (100%)	0	100	100
1	L	65/69 (94%)	65 (100%)	0	100	100
All	All	779/828 (94%)	773 (99%)	6 (1%)	85	88

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	34	LEU
1	H	51	PRO
1	D	51	PRO
1	A	55	LYS

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Mol	Chain	Res	Type
1	E	55	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	35	GLN
1	L	73	GLN
1	I	48	GLN
1	D	16	GLN
1	H	16	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.